mRNA/sRNA transcription, DNA methylation, histone modifications, and engaged RNA polymerase activity. These were integrated with genome-wide polymorphism and divergence data from 1,477 rice accessions and 11 reference genome sequences in the *Oryzeae*. We found ρ to be multimodal, with ~9% of the rice genome falling into classes where more than half of the bases would likely have a fitness consequence if mutated. Around 2% of the rice genome showed evidence of weak negative selection, frequently at candidate regulatory sites, including a novel set of 1,000 potentially active enhancer elements. This fitness consequence map provides perspective on the evolutionary forces associated with genome diversity, aids in genome annotation, and can guide crop breeding programs.

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South Green Resources to Manage Rice Big Genomics Data

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We have developed the Rice Genome Hub, an integrative genome information system that allows centralized access to genomics and genetics data, and analytical tools to facilitate translational and applied research in rice. The hub is built using the Content Management System Drupal with the Tripal module that interacts with the Chado database. The Hub interface provides several functionalities (Blast, DotPlots, Gene Search, JBrowse, Primer Blaster, Primer Designer) to make it easy for querying, visualizing and downloading research data. We also plugged in-house tools developed by the South Green bioinformatics platform.

Among these tools, Gigwa is a Web-based tool which provides an easy and intuitive way to explore large amounts of genotyping data by filtering the latter based not only on variant features, including functional annotations, but also on genotype patterns.

We also developed RedOak, a reference-free and alignment-free software package that allows for the indexing of a large collection of similar genomes. RedOak can be applied to reads from unassembled genomes, and it provides a nucleotide sequence query function. This software is based on a k-mer approach and has been developed to be heavily parallelized and distributed on several nodes of a cluster. Analysis of presence-absence variation (PAV) of genes among different genomes is a classical output of pan-genomic approaches. RedOak has a nucleotide sequence query function, including reverse complements, that can be used to quickly analyze the PAV of a specific gene among a large collection of genomes.

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Planteome: Ontologies and Resources for Integrative Plant Genomics

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The Planteome Project (www.planteome.org) provides semantic integration of plant genomics datasets and reference ontologies describing domains in plant biology (plant anatomy, development, phenotypes, traits, growing conditions and treatments, plant stresses) across 95 plant species. The Planteome also hosts external reference ontologies, as well as species-specific Crop Ontologies developed by plant breeding and research communities from around the world.The latest release, Version 3.0 of the project database includes more than two million bioentities (data objects), with more than 21 million associations between bioetities and ontology terms. The online database and APIs provide researchers with tools to access resources for plant traits, phenotypes, diseases, genomes, gene expression and genetic